Amendments to the Claims:

Applicants submit that claims 1-46 and 106-112 have been cancelled previously. Prior to further substantive examination, please cancel pending claims 47-75, 77 and 78 without prejudice to their subsequent reintroduction into this application or their introduction into another application. Claims 76, 79, 101 and 102 have been amended. The following list of claims replaces all prior versions and lists of claims in the application:

Listing of Claims:

1-75 (Cancelled)

76. (Currently Amended) A method of identifying a candidate molecule, the method comprising the steps of:

(a) providing a molecular model of a ribofunctional locus of a large subunit of a ribosome, wherein the molecular model is based on atoms derived from an electron density map having a resolution of at least about 4.5 Å; and

(b) using the model to identify a candidate molecule capable of having ~~a surface complementary~~ binding specificity for ~~to~~ the ribofunctional locus; and

(c) producing the candidate molecule identified in step (b).

77. (Cancelled)

78. (Cancelled)

79. (Currently Amended) The method of claim 76 ~~or 78~~, comprising the additional step of determining whether the candidate molecule modulates ribosomal activity.

80. (Currently Amended) The method of claim 79, comprising the additional step of repeating step (b) to identify ~~identifying~~ a modified molecule.

81. (Original) The method of claim 80, comprising the additional step of producing the modified molecule.

82. (Original) The method of claim 81, comprising the additional step of determining whether the modified molecule modulates ribosomal activity.

83. (Original) The method of claim 82, comprising the additional step of producing the modified molecule.

84. (Currently Amended) The method of claim 76, wherein the candidate molecule is an antibiotic ~~or an antibiotic analogue~~.

85. (Currently Amended) The method of claim 80, wherein the modified molecule is an antibiotic ~~or an antibiotic analogue~~.

86. (Currently Amended) The method of claim 84, wherein the antibiotic ~~or antibiotic analogue~~ is a macrolide.

87. (Original) The method of claim 76, wherein the ribofunctional locus comprises at least a portion of an active site.

88. (Original) The method of claim 87, wherein the active site comprises at least a portion of a peptidyl transferase site.

89. (Original) The method of claim 87, wherein the peptidyl transferase site is defined by a plurality of residues set forth in Table 5.

90. (Original) The method of claim 76, wherein the ribofunctional locus comprises at least a portion of an A-site.

91. (Original) The method of claim 90, wherein the A-site is defined by a plurality of residues set forth in Table 6.

92. (Original) The method of claim 76 or 90, wherein the ribofunctional locus comprises a least a portion of a P-site.

93. (Original) The method of claim 92, wherein the P-site is defined by a plurality of residues set forth in Table 7.

94. (Original) The method of claim 76 or 90, wherein the ribofunctional locus comprises at least a portion of a polypeptide exit tunnel.

95. (Original) The method of claim 94, wherein the exit tunnel is defined by a plurality of residues set forth in Table 8, Table 9 or Table 10.

96. (Original) The method of claim 92, wherein the ribofunctional locus comprises at least a portion of a polypeptide exit tunnel.

97. (Original) The method of claim 96, wherein the exit tunnel is defined by a plurality of residues set forth in Table 8, Table 9 or Table 10.

98. (Original) The method of claim 76, wherein the ribofunctional locus is defined by a plurality of residues set forth in Table 11, Table 12, Table 13, Table 14, Table 15, Table 16 or Table 17.

99. (Original) The method of claim 76, wherein the molecular model is in an electronic form.

100. (Original) The method of claim 76, wherein the molecular model is generated from atomic co-ordinates produced by molecular modeling.

101. (Currently Amended) The method of claim 76 or 100, wherein the molecular model is generated from atomic co-ordinates produced by homology modeling using at least a portion of the atomic co-ordinates ~~deposited at the Protein Data Bank under accession number PDB ID: 1FFK, 1FFZ, 1FG0, or 1JJ2~~ recorded on Disk No. 1 of 3 under file name 1ffk.doc, 1ffz.doc, or 1fg0.doc or on Disk No. 2 of 3 under file name 1jj2.rtf.

102. (Currently Amended) The method of claim 76 or 100, wherein the molecular model is generated from atomic co-ordinates produced by molecular replacement using at least a portion of the atomic co-ordinates ~~deposited at the Protein Data Bank under accession number PDB ID: 1FFK, 1FFZ, 1FG0, or 1JJ2~~ recorded on Disk No. 1 of 3 under file name 1ffk.doc, 1ffz.doc, or 1fg0.doc or on Disk No. 2 of 3 under file name 1jj2.rtf.

103. (Original) The method of claim 76, wherein the molecular model comprises residues that are conserved among prokaryotic organisms.

104. (Original) The method of claim 76, wherein the molecular model comprises a residue that is present in a prokaryotic ribosome but is absent from a eukaryotic ribosome.

105. (Original) The method of claim 104, wherein the eukaryotic ribosome is a mammalian ribosome.

106-112 (Cancelled)